

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/840,704

DATE: 12/19/2001

TIME: 13:05:37

Input Set : N:\Crf3\RULE60\09840704.raw

Output Set: N:\CRF3\12192001\I840704.raw

OIPE

H-5
4-3-02
P.2

1 <110> APPLICANT: Dedhar, Shoukat
 2 Hannigan, Greg
 3 <120> TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
 4 <130> FILE REFERENCE: KIN-2CON
 5 <140> CURRENT APPLICATION NUMBER: 09/840,704
 6 <141> CURRENT FILING DATE: 2001-04-23
 7 <150> PRIOR APPLICATION NUMBER: 09/566,906
 8 <151> PRIOR FILING DATE: 2000-05-09
 9 <150> PRIOR APPLICATION NUMBER: US08/752,345
 10 <151> PRIOR FILING DATE: 1996-11-19
 11 <160> NUMBER OF SEQ ID NOS: 16
 12 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 1789
 16 <212> TYPE: DNA
 17 <213> ORGANISM: H. sapiens
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (157)...(1512)
 W--> 21 <221> NAME/KEY: Other
 22 <222> LOCATION: (0)...(0)
 23 <400> SEQUENCE: 1

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TECH CENTER 1600/2900

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24	gaattcatct gtcgactgct accacgggag ttccccggag aaggatctg cagcccgagt	60
25	cccgaggata aagcttgggg ttcatctctc ttccctggat cactccacag tcctcaggct	120
26	tccccaatcc aggggactcg gcgcccggac gctgct atg	174
27	Met Asp Asp Ile Phe Thr	
28	1 5	
29	cag tgc cgg gag ggc aac gca gtc gcc gtt cgc ctg tgg ctg gac aac	222
30	Gln Cys Arg Glu Gly Asn Ala Val Ala Val Arg Leu Trp Leu Asp Asn	
31	10 15 20	
32	acg gag aac gac ctc aac cag ggg gac gat cat ggc ttc tcc ccc ttg	270
33	Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp His Gly Phe Ser Pro Leu	
34	25 30 35	
35	cac tgg gcc tgc cga gag ggc cgc tct gct gtg gtt gag atg ttg atc	318
36	His Trp Ala Cys Arg Glu Gly Arg Ser Ala Val Val Glu Met Leu Ile	
37	40 45 50	
38	atg cgg ggg gca cgg atc aat gta atg aac cgt ggg gat gac acc ccc	366
39	Met Arg Gly Ala Arg Ile Asn Val Met Asn Arg Gly Asp Asp Thr Pro	
40	55 60 65 70	
41	ctg cat ctg gca gcc agt cat gga cac cgt gat att gta cag aag cta	414
42	Leu His Leu Ala Ala Ser His Gly His Arg Asp Ile Val Gln Lys Leu	
43	75 80 85	
44	ttg cag tac aag gca gac atc aat gca gtg aat gaa cac ggg aat gtg	462
45	Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val Asn Glu His Gly Asn Val	
46	90 95 100	
47	ccc ctg cac tat gcc tgt ttt tgg ggc caa gat caa gtg gca gag gac	510
48	Pro Leu His Tyr Ala Cys Phe Trp Gly Gln Asp Gln Val Ala Glu Asp	

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49	105						110						115						
50	ctg	gtg	gca	aat	ggg	gcc	ctt	gtc	agc	atc	tgt	aac	aag	tat	gga	gag	558		
51	Leu	Val	Ala	Asn	Gly	Ala	Leu	Val	Ser	Ile	Cys	Asn	Lys	Tyr	Gly	Glu			
52	120						125						130						
53	atg	cct	gtg	gac	aaa	gcc	aag	gca	ccc	ctg	aga	gag	ctt	ctc	cga	gag	606		
54	Met	Pro	Val	Asp	Lys	Ala	Lys	Ala	Pro	Leu	Arg	Glu	Leu	Leu	Arg	Glu			
55	135						140						145						150
56	cgg	gca	gag	aag	atg	ggc	cag	aat	ctc	aac	cgt	att	cca	tac	aag	gac	654		
57	Arg	Ala	Glu	Lys	Met	Gly	Gln	Asn	Leu	Asn	Arg	Ile	Pro	Tyr	Lys	Asp			
58	155						160						165						
59	aca	ttc	tggt	aag	ggg	acc	acc	cgc	act	cgg	ccc	cga	aat	gga	acc	ctg	702		
60	Thr	Phe	Trp	Lys	Gly	Thr	Thr	Arg	Thr	Arg	Pro	Arg	Asn	Gly	Thr	Leu			
61	170						175						180						
62	aac	aaa	cac	tct	ggc	att	gac	ttc	aaa	cag	ctt	aac	ttc	ctg	acg	aag	750		
63	Asn	Lys	His	Ser	Gly	Ile	Asp	Phe	Lys	Gln	Leu	Asn	Phe	Leu	Thr	Lys			
64	185						190						195						
65	ctc	aac	gag	aat	cac	tct	gga	gag	cta	tggt	aag	ggc	cgc	tggt	cag	ggc	798		
66	Leu	Asn	Glu	Asn	His	Ser	Gly	Glu	Leu	Trp	Lys	Gly	Arg	Trp	Gln	Gly			
67	200						205						210						
68	aat	gac	att	gtc	gtg	aag	gtg	ctg	aag	gtt	cga	gac	tggt	agt	aca	agg	846		
69	Asn	Asp	Ile	Val	Val	Lys	Val	Leu	Lys	Val	Arg	Asp	Trp	Ser	Thr	Arg			
70	215						220						225						230
71	aag	agc	agg	gac	ttc	aat	gaa	gag	tgt	ccc	cgg	ctc	agg	att	ttc	tcg	894		
72	Lys	Ser	Arg	Asp	Phe	Asn	Glu	Glu	Cys	Pro	Arg	Leu	Arg	Ile	Phe	Ser			
73	235						240						245						
74	cat	cca	aat	gtg	ctc	cca	gtg	cta	ggt	gcc	tgc	cag	tct	cca	cct	gct	942		
75	His	Pro	Asn	Val	Leu	Pro	Val	Leu	Gly	Ala	Cys	Gln	Ser	Pro	Pro	Ala			
76	250						255						260						
77	cct	cat	cct	act	ctc	atc	aca	cac	tggt	atg	ccg	tat	gga	tcc	ctc	tac	990		
78	Pro	His	Pro	Thr	Leu	Ile	Thr	His	Trp	Met	Pro	Tyr	Gly	Ser	Leu	Tyr			
79	265						270						275						
80	aat	gta	cta	cat	gaa	ggc	acc	aat	ttc	gtc	gtg	gac	cag	agc	cag	gct	1038		
81	Asn	Val	Leu	His	Glu	Gly	Thr	Asn	Phe	Val	Val	Asp	Gln	Ser	Gln	Ala			
82	280						285						290						
83	gtg	aag	ttt	gct	ttg	gac	atg	gca	agg	ggc	atg	gcc	ttc	cta	cac	aca	1086		
84	Val	Lys	Phe	Ala	Leu	Asp	Met	Ala	Arg	Gly	Met	Ala	Phe	Leu	His	Thr			
85	295						300						305						310
86	cta	gag	ccc	ctc	atc	cca	cga	cat	gca	ctc	aat	agc	cgt	agt	gta	atg	1134		
87	Leu	Glu	Pro	Leu	Ile	Pro	Arg	His	Ala	Leu	Asn	Ser	Arg	Ser	Val	Met			
88	315						320						325						
89	att	gat	gag	gac	atg	act	gcc	cga	att	agc	atg	gct	gat	gtc	aag	ttc	1182		
90	Ile	Asp	Glu	Asp	Met	Thr	Ala	Arg	Ile	Ser	Met	Ala	Asp	Val	Lys	Phe			
91	330						335						340						
92	tct	tt																	

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98      atg tgg agt ttt gca gtg ctt ctg tgg gaa ctg gtg aca cgg gag gta      1326
99      Met Trp Ser Phe Ala Val Leu Leu Trp Glu Leu Val Thr Arg Glu Val
100      375                      380                      385                      390
101      ccc ttt gct gac ctc tcc aat atg gag att gga atg aag gtg gca ttg      1374
102      Pro Phe Ala Asp Leu Ser Asn Met Glu Ile Gly Met Lys Val Ala Leu
103                      395                      400                      405
104      gaa ggc ctt cgg cct acc atc cca cca ggt att tcc cct cat gtg tgt      1422
105      Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly Ile Ser Pro His Val Cys
106                      410                      415                      420
107      aag ctc atg aag atc tgc atg aat gaa gac cct gca aag cga ccc aaa      1470
108      Lys Leu Met Lys Ile Cys Met Asn Glu Asp Pro Ala Lys Arg Pro Lys
109                      425                      430                      435
110      ttt gac atg att gtg cct atc ctt gag aag atg cag gac aag      1512
111      Phe Asp Met Ile Val Pro Ile Leu Glu Lys Met Gln Asp Lys
112      440                      445                      450
113      taggactgga aggtccttgc ctgaactcca gaggtgtcgg gacatggttg ggggaatgca      1572
114      cctcccaaaa gcagcaggcc tctggttgcc tccccgcct ccagtcattg tactaccca      1632
115      gcctgggggc catccccttc ccccatccct accactgtgc gcaagagggg cgggctcaga      1692
116      gctttgtcac ttgccacatg gtgtctccca acatggggagg gatcagcccc gcctgtcaca      1752
117      ataaagttta ttatgaaaaa aaaaaaaaaa aaaaaaaa      1789
119 <210> SEQ ID NO: 2
120 <211> LENGTH: 452
121 <212> TYPE: PRT
122 <213> ORGANISM: H. sapiens
123 <400> SEQUENCE: 2
124      Met Asp Asp Ile Phe Thr Gln Cys Arg Glu Gly Asn Ala Val Ala Val
125      1                      5                      10                      15
126      Arg Leu Trp Leu Asp Asn Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp
127      20                      25                      30
128      His Gly Phe Ser Pro Leu His Trp Ala Cys Arg Glu Gly Arg Ser Ala
129      35                      40                      45
130      Val Val Glu Met Leu Ile Met Arg Gly Ala Arg Ile Asn Val Met Asn
131      50                      55                      60
132      Arg Gly Asp Asp Thr Pro Leu His Leu Ala Ala Ser His Gly His Arg
133      65                      70                      75                      80
134      Asp Ile Val Gln Lys Leu Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val
135      85                      90                      95
136      Asn Glu His Gly Asn Val Pro Leu His Tyr Ala Cys Phe Trp Gly Gln
137      100                     105                     110
138      Asp Gln Val Ala Glu Asp Leu Val Ala Asn Gly Ala Leu Val Ser Ile
139      115                     120                     125
140      Cys Asn Lys Tyr Gly Glu Met Pro Val Asp Lys Ala Lys Ala Pro Leu
141      130                     135                     140
142      Arg Glu Leu Leu Arg Glu Arg Ala Glu Lys Met Gly Gln Asn Leu Asn
143      145                     150                     155                     160
144      Arg Ile Pro Tyr Lys Asp Thr Phe Trp Lys Gly Thr Thr Arg Thr Arg
145      165                     170                     175
146      Pro Arg Asn Gly Thr Leu Asn Lys His Ser Gly Ile Asp Phe Lys Gln
147      180                     185                     190

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```

148   Leu Asn Phe Leu Thr Lys Leu Asn Glu Asn His Ser Gly Glu Leu Trp
149           195                200                205
150   Lys Gly Arg Trp Gln Gly Asn Asp Ile Val Val Lys Val Leu Lys Val
151           210                215                220
152   Arg Asp Trp Ser Thr Arg Lys Ser Arg Asp Phe Asn Glu Glu Cys Pro
153   225                230                235                240
154   Arg Leu Arg Ile Phe Ser His Pro Asn Val Leu Pro Val Leu Gly Ala
155           245                250                255
156   Cys Gln Ser Pro Pro Ala Pro His Pro Thr Leu Ile Thr His Trp Met
157           260                265                270
158   Pro Tyr Gly Ser Leu Tyr Asn Val Leu His Glu Gly Thr Asn Phe Val
159           275                280                285
160   Val Asp Gln Ser Gln Ala Val Lys Phe Ala Leu Asp Met Ala Arg Gly
161           290                295                300
162   Met Ala Phe Leu His Thr Leu Glu Pro Leu Ile Pro Arg His Ala Leu
163   305                310                315                320
164   Asn Ser Arg Ser Val Met Ile Asp Glu Asp Met Thr Ala Arg Ile Ser
165           325                330                335
166   Met Ala Asp Val Lys Phe Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala
167           340                345                350
168   Pro Ala Trp Val Ala Pro Glu Ala Leu Gln Lys Lys Pro Glu Asp Thr
169           355                360                365
170   Asn Arg Arg Ser Ala Asp Met Trp Ser Phe Ala Val Leu Leu Trp Glu
171           370                375                380
172   Leu Val Thr Arg Glu Val Pro Phe Ala Asp Leu Ser Asn Met Glu Ile
173   385                390                395                400
174   Gly Met Lys Val Ala Leu Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly
175           405                410                415
176   Ile Ser Pro His Val Cys Lys Leu Met Lys Ile Cys Met Asn Glu Asp
177           420                425                430
178   Pro Ala Lys Arg Pro Lys Phe Asp Met Ile Val Pro Ile Leu Glu Lys
179           435                440                445
180   Met Gln Asp Lys
181           450

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183 <210> SEQ ID NO: 3

184 <211> LENGTH: 258

185 <212> TYPE: PRT

186 <213> ORGANISM: H. sapiens

187 <220> FEATURE:

W--> 188 <221> NAME/KEY: Other

189 <222> LOCATION: (1)...(258)

190 <400> SEQUENCE: 3

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191   Asn Met Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe
192   1                5                10                15
193   Gly Asp Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys
194           20                25                30
195   Cys Ile Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser
196           35                40                45
197   Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val

```

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Output Set: N:\CRF3\12192001\I840704.raw

```

198          50          55          60
199 Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala
200 65          70          75          80
201 Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu
202          85          90          95
203 Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met
204          100          105          110
205 Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg
206          115          120          125
207 Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly
208          130          135          140
209 Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val
210          145          150          155          160
211 Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys
212          165          170          175
213 Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe
214          180          185          190
215 Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg
216          195          200          205
217 Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala
218          210          215          220
219 Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg
220          225          230          235          240
221 Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His
222          245          250          255
223 Glu Leu
225 <210> SEQ ID NO: 4
226 <211> LENGTH: 256
227 <212> TYPE: PRT
228 <213> ORGANISM: H. sapiens
229 <220> FEATURE:
W--> 230 <221> NAME/KEY: Other
231 <222> LOCATION: (1)...(256)
232 <400> SEQUENCE: 4
233 Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys
234 1          5          10          15
235 Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala
236          20          25          30
237 Ile Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln
238          35          40          45
239 Glu Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu
240          50          55          60
241 Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met
242          65          70          75          80
243 Thr Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Glu Gly Lys Phe
244          85          90          95
245 Leu Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly
246          100          105          110
247 Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala

```

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09840704.raw

Output Set: N:\CRF3\12192001\I840704.raw

L:21 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:188 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:230 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:271 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:314 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:357 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:367 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12